Homework 5: Models and Model Comparisons

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Task 1: Conceptual Questions

- What is the purpose of using cross-validation when fitting a random forest model?

Generally, when fitting a random forest model, we want to randomly subset predictors to make sure that no predictor overwhelms the model and significantly effects the output. As such, we need to choose how many predictors are subset each time. This is where cross-validation comes into play. By implementing cross-validation and obtaining the most optimized tuning parameter we can improve our predictions.

- Describe the bagged tree algorithm.

In the bagged tree algorithm, we begin by bootstrapping some number of samples B. From there, we can fit a tree to each sample to have B number of trees. Then, from there, we can find response for each tree and then combine them to aggregate a final prediction. In practice, this combination is typically the average of all the sample predictions.

- What is meant by general linear model?

A general linear model is the family of models that we use more conventionally. For example, SLRs, MLRs, ANOVA and ANCOVA models all fall under this family (so long as all effects are fixed and not random). The main characteristic of these models is assuming that the response variable follows a normal distribution.

- When fitting a multiple linear regression model, what does adding an interaction term do? That is, what does it allow the model to do differently as compared to when it is not included in the model?

The main reason to include an interaction variable is to allow the effect of one variable to be dependent on another variable. For example, in a plant growth study, the amount of sunlight and temperature may be heavily related to one another, so an interaction term may be beneficial to include in the model.

- Why do we split our data into a training and test set?

Splitting the model into a training set and test set allows us to see how well the model may perform if it was tasked with prediction future observations. By having test data, we can compare a model's predictions to the actual outcome to measure performance.

Task 2: Data Prep

Packages and Data

```
library(tidyverse)
library(tidymodels)
library(caret)
library(yardstick)

heart <- as_tibble(read.csv("heart.csv", header = TRUE))
```

Question 1

```
summary(heart)
```

```
      Age            Sex            ChestPainType        RestingBP
 Min.   :28.00   Length:918         Length:918         Min.   :  0.0
 1st Qu.:47.00   Class :character   Class :character   1st Qu.:120.0
 Median :54.00   Mode  :character   Mode  :character   Median :130.0
 Mean   :53.51                                         Mean   :132.4
 3rd Qu.:60.00                                         3rd Qu.:140.0
 Max.   :77.00                                         Max.   :200.0
  Cholesterol      FastingBS       RestingECG            MaxHR
 Min.   :  0.0   Min.   :0.0000   Length:918         Min.   : 60.0
 1st Qu.:173.2   1st Qu.:0.0000   Class :character   1st Qu.:120.0
 Median :223.0   Median :0.0000   Mode  :character   Median :138.0
 Mean   :198.8   Mean   :0.2331                      Mean   :136.8
 3rd Qu.:267.0   3rd Qu.:0.0000                      3rd Qu.:156.0
 Max.   :603.0   Max.   :1.0000                      Max.   :202.0
 ExerciseAngina        Oldpeak          ST_Slope          HeartDisease
 Length:918         Min.   :-2.6000   Length:918         Min.   :0.0000
 Class :character   1st Qu.: 0.0000   Class :character   1st Qu.:0.0000
 Mode  :character   Median : 0.6000   Mode  :character   Median :1.0000
                    Mean   : 0.8874                      Mean   :0.5534
```

```
 3rd Qu.: 1.5000                      3rd Qu.:1.0000
 Max.   : 6.2000                      Max.   :1.0000
```

The `HeartDisease` variable is quantitative. This does not make sense, since an individual either has a heart disease or they don't, so it is more intuitive to consider this a categorical variable.

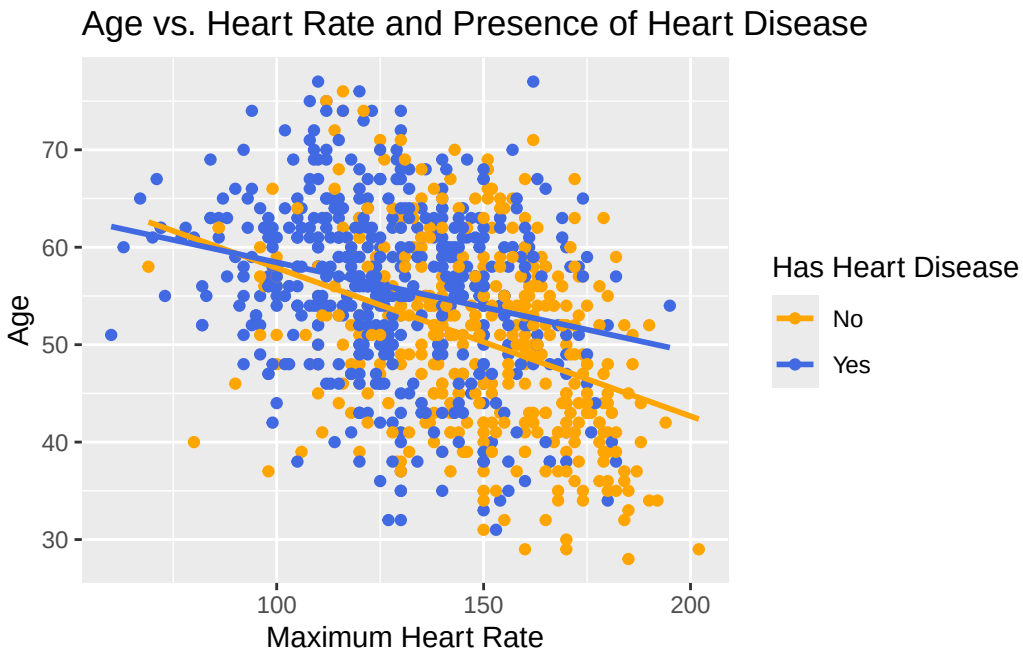
Question 2

```
#Subset dataset into relevant data of the correct type

heart_new <- heart |>
  mutate(HasHeartDisease = as.factor(HeartDisease)) |>
  select(-c(ST_Slope, HeartDisease))

#Change names of factor levels in HasHeartDisease to improve plot outputs later down the line

levels(heart_new$HasHeartDisease) <- c("No", "Yes")
```

Task 3: EDA

Question 1

```
#Plot Age vs. Heart Rate, grouped by Heart Disease status

ggplot(data = heart_new, aes(x = MaxHR, y = Age, color = HasHeartDisease)) +
  geom_point() +
  geom_smooth(method = lm, se = FALSE, formula = y ~ x) +
  labs(x = "Maximum Heart Rate", y = "Age", title = "Age vs. Heart Rate and Presence of Heart
  scale_color_manual(values = c("orange", "royalblue"))
```



Question 2

Based on our output above, it looks like the presence of heart disease makes a sizable impact on the regression line. As such, an interaction term appears necessary as heart disease may have a notable effect on an individuals maximum heart rate.

Task 4: Testing and Training

```
#Set random seed so results are reproducible
set.seed(101)

#Split data into a testing set and training set
heart_split <- initial_split(heart_new, prop = 0.8)
test <- testing(heart_split)
train <- training(heart_split)
```